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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=12; day=20; hr=11; min=36; sec=40; ms=752;  
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Application No: 10584424 Version No: 2.0

**Input Set:**

**Output Set:**

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**Finished:** 2011-12-12 13:25:02.321  
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**Total Warnings:** 68  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 80  
**Actual SeqID Count:** 80

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**Input Set:**

**Output Set:**

**Started:** 2011-12-12 13:24:59.439  
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Error code      Error Description

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Shuttleworth, Gillian  
Finnis, Christopher John Arthur

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35 40 45

His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys  
50 55 60

Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu  
65 70 75 80

Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu  
85 90 95

Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys  
100 105 110

Asn Ser Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala  
115 120 125

Glu Ala Ile Val Gln Phe Met Ile Lys Gln Ser Gln Pro Ala Val Ala  
130 135 140

Val Val Ala Asp Leu Pro Ala Tyr Leu Ala Asn Glu Thr Phe Val Thr  
145 150 155 160

Pro Val Ile Val Gln Ser Gly Lys Ile Asp Ala Asp Phe Asn Ala Thr  
165 170 175

Phe Tyr Ser Met Ala Asn Lys His Phe Asn Asp Tyr Asp Phe Val Ser  
180 185 190

Ala Glu Asn Ala Asp Asp Asp Phe Lys Leu Ser Ile Tyr Leu Pro Ser  
195 200 205

Ala Met Asp Glu Pro Val Val Tyr Asn Gly Lys Lys Ala Asp Ile Ala  
210 215 220

Asp Ala Asp Val Phe Glu Lys Trp Leu Gln Val Glu Ala Leu Pro Tyr  
225 230 235 240

Phe Gly Glu Ile Asp Gly Ser Val Phe Ala Gln Tyr Val Glu Ser Gly  
245 250 255

Leu Pro Leu Gly Tyr Leu Phe Tyr Asn Asp Glu Glu Glu Leu Glu Glu  
260 265 270

Tyr Lys Pro Leu Phe Thr Glu Leu Ala Lys Lys Asn Arg Gly Leu Met  
275 280 285

Asn Phe Val Ser Ile Asp Ala Arg Lys Phe Gly Arg His Ala Gly Asn  
290 295 300

Leu Asn Met Lys Glu Gln Phe Pro Leu Phe Ala Ile His Asp Met Thr  
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Glu Asp Leu Lys Tyr Gly Leu Pro Gln Leu Ser Glu Glu Ala Phe Asp  
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Glu Leu Ser Asp Lys Ile Val Leu Glu Ser Lys Ala Ile Glu Ser Leu  
340 345 350

Val Lys Asp Phe Leu Lys Gly Asp Ala Ser Pro Ile Val Lys Ser Gln  
355 360 365

Glu Ile Phe Glu Asn Gln Asp Ser Ser Val Phe Gln Leu Val Gly Lys  
370 375 380

Asn His Asp Glu Ile Val Asn Asp Pro Lys Lys Asp Val Leu Val Leu  
385 390 395 400

Tyr Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Thr Tyr  
405 410 415

Gln Glu Leu Ala Asp Thr Tyr Ala Asn Ala Thr Ser Asp Val Leu Ile  
420 425 430

Ala Lys Leu Asp His Thr Glu Asn Asp Val Arg Gly Val Val Ile Glu  
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Gly Tyr Pro Thr Ile Val Leu Tyr Pro Gly Gly Lys Ser Glu Ser  
450 455 460

Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile  
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Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu  
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Asp Glu Glu Asp Ala Ile His Asp Glu Leu  
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<212> PRT  
<213> *Saccharomyces cerevisiae*

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Ala Val Val Lys Leu Ala Thr Asp Ser Phe Asn Glu Tyr Ile Gln Ser			
35	40	45	
His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys			
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Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu			
65	70	75	80
Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu			
85	90	95	
Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys			
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Asn Arg Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala			
115	120	125	
Glu Ala Ile Val Gln Phe Met Ile Lys Gln Ser Gln Pro Ala Val Ala			
130	135	140	
Val Val Ala Asp Leu Pro Ala Tyr Leu Ala Asn Glu Thr Phe Val Thr			
145	150	155	160
Pro Val Ile Val Gln Ser Gly Lys Ile Asp Ala Asp Phe Asn Ala Thr			
165	170	175	
Phe Tyr Ser Met Ala Asn Lys His Phe Asn Asp Tyr Asp Phe Val Ser			
180	185	190	
Ala Glu Asn Ala Asp Asp Asp Phe Lys Leu Ser Ile Tyr Leu Pro Ser			
195	200	205	
Ala Met Asp Glu Pro Val Val Tyr Asn Gly Lys Lys Ala Asp Ile Ala			
210	215	220	
Asp Ala Asp Val Phe Glu Lys Trp Leu Gln Val Glu Ala Leu Pro Tyr			
225	230	235	240

Phe Gly Glu Ile Asp Gly Ser Val Phe Ala Gln Tyr Val Glu Ser Gly  
245 250 255

Leu Pro Leu Gly Tyr Leu Phe Tyr Asn Asp Glu Glu Glu Leu Glu Glu  
260 265 270

Tyr Lys Pro Leu Phe Thr Glu Leu Ala Lys Lys Asn Arg Gly Leu Met  
275 280 285

Asn Phe Val Ser Ile Asp Ala Arg Lys Phe Gly Arg His Ala Gly Asn  
290 295 300

Leu Asn Met Lys Glu Gln Phe Pro Leu Phe Ala Ile His Asp Met Thr  
305 310 315 320

Glu Asp Leu Lys Tyr Gly Leu Pro Gln Leu Ser Glu Glu Ala Phe Asp  
325 330 335

Glu Leu Ser Asp Lys Ile Val Leu Glu Ser Lys Ala Ile Glu Ser Leu  
340 345 350

Val Lys Asp Phe Leu Lys Gly Asp Ala Ser Pro Ile Val Lys Ser Gln  
355 360 365

Glu Ile Phe Glu Asn Gln Asp Ser Ser Val Phe Gln Leu Val Gly Lys  
370 375 380

Asn His Asp Glu Ile Val Asn Asp Pro Lys Lys Asp Val Leu Val Leu  
385 390 395 400

Tyr Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Thr Tyr  
405 410 415

Gln Glu Leu Ala Asp Thr Tyr Ala Asn Ala Thr Ser Asp Val Leu Ile  
420 425 430

Ala Lys Leu Asp His Thr Glu Asn Asp Val Arg Gly Val Val Ile Glu  
435 440 445

Gly Tyr Pro Thr Ile Val Leu Tyr Pro Gly Gly Lys Lys Ser Glu Ser  
450 455 460

Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile  
465 470 475 480

Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu  
485 490 495

Ala Gln Glu Lys Ala Ala Glu Glu Ala Asp Ala Glu Ala Glu  
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Ala Asp Ala Asp Ala Glu Leu Ala Asp Glu Glu Asp Ala Ile His Asp  
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Glu Leu  
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Asn Arg Thr Thr Pro Ser Phe Val Ala Phe Thr Asp Thr Glu Arg Leu  
35 40 45

Ile Gly Asp Ala Ala Lys Asn Gln Ala Ala Met Asn Pro Ser Asn Thr  
50 55 60

Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Asn Phe Asn Asp Pro Glu  
65 70 75 80

Val Gln Ala Asp Met Lys His Phe Pro Phe Lys Leu Ile Asp Val Asp  
85 90 95

Gly Lys Pro Gln Ile Gln Val Glu Phe Lys Gly Glu Thr Lys Asn Phe  
100 105 110

Thr Pro Glu Gln Ile Ser Ser Met Val Leu Gly Lys Met Lys Glu Thr  
115 120 125

Ala Glu Ser Tyr Leu Gly Ala Lys Val Asn Asp Ala Val Val Thr Val  
130 135 140

Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly  
145 150 155 160

Thr Ile Ala Gly Leu Asn Val Leu Arg Ile Ile Asn Glu Pro Thr Ala  
165 170 175

Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys Gly Lys Glu Glu His Val  
180 185 190

Leu Ile Phe Asp Leu Gly Gly Thr Phe Asp Val Ser Leu Leu Phe  
195 200 205

Ile Glu Asp Gly Ile Phe Glu Val Lys Ala Thr Ala Gly Asp Thr His  
210 215 220

Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu Val Asn His Phe Ile Gln  
225 230 235 240

Glu Phe Lys Arg Lys Asn Lys Lys Asp Leu Ser Thr Asn Gln Arg Ala  
245 250 255

Leu Arg Arg Leu Arg Thr Ala Cys Glu Arg Ala Lys Arg Thr Leu Ser  
260 265 270

Ser Ser Ala Gln Thr Ser Val Glu Ile Asp Ser Leu Phe Glu Gly Ile  
275 280 285

Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu Leu Cys Ala  
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Asp Leu Phe Arg Ser Thr Leu Asp Pro Val Glu Lys Val Leu Arg Asp  
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Ala Lys Leu Asp Lys Ser Gln Val Asp Glu Ile Val Leu Val Gly Gly  
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Ser Thr Arg Ile Pro Lys Val Gln Lys Leu Val Thr Asp Tyr Phe Asn  
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Gly Lys Glu Pro Asn Arg Ser Ile Asn Pro Asp Glu Ala Val Ala Tyr  
355 360 365

Gly Ala Ala Val Gln Ala Ala Ile Leu Thr Gly Asp Glu Ser Ser Lys  
370 375 380

Thr Gln Asp Leu Leu Leu Asp Val Ala Pro Leu Ser Leu Gly Ile  
385 390 395 400

Glu Thr Ala Gly Gly Val Met Thr Lys Leu Ile Pro Arg Asn Ser Thr  
405 410 415

Ile Ser Thr Lys Lys Phe Glu Ile Phe Ser Thr Tyr Ala Asp Asn Gln  
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Pro Gly Val Leu Ile Gln Val Phe Glu Gly Glu Arg Ala Lys Thr Lys  
435 440 445

Asp Asn Asn Leu Leu Gly Lys Phe Glu Leu Ser Gly Ile Pro Pro Ala  
450 455 460

Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Val Asp Ser Asn  
465 470 475 480

Gly Ile Leu Asn Val Ser Ala Val Glu Lys Gly Thr Gly Lys Ser Asn  
485 490 495

Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys Glu Asp Ile  
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Glu Lys Met Val Ala Glu Ala Glu Lys Phe Lys Glu Glu Asp Glu Lys  
515 520 525

Glu Ser Gln Arg Ile Ala Ser Lys Asn Gln Leu Glu Ser Ile Ala Tyr  
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Ser Leu Lys Asn Thr Ile Ser Glu Ala Gly Asp Lys Leu Glu Gln Ala  
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Asp Lys Asp Thr Val Thr Lys Lys Ala Glu Glu Thr Ile Ser Trp Leu  
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Asp Ser Asn Thr Thr Ala Ser Lys Glu Glu Phe Asp Asp Lys Leu Lys  
580 585 590

Glu Leu Gln Asp Ile Ala Asn Pro Ile Met Ser Lys Leu Tyr Gln Ala  
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Gly Gly Ala Pro Pro Ala Pro Glu Ala Glu Gly Pro Thr Val Glu Glu  
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